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Substitute for form 1449A/PTO INFORMATION DISCLOSURE STATEMENT BY APPLICANT (use as many sheets as necessary)		Complete if Known			
		Application Number	10/090,698		
		Filing Date	March 4, 2002		
		First Named Inventor	MURRAY et al.		
		Group Art Unit	1637		
		Examiner Name			
Sheet	1	of	3	Attorney Docket Number	AGYT-011CIP

U.S. PATENT DOCUMENTS						
Examiner Initials ¹	Cite No. ¹	U.S. Patent Documents		Name of Patentee or Applicant of Cited Documents	Date of Publication of Cited Document MM-DD-YYYY	Pages, columns, lines, Where Relevant Passages or Relevant Figures Appear
		Number	Kind Code ² (if known)			
JP		5,593,839		Hubbell, et al.	01-14-1997	
JP		5,807,522		Brown, et al.	09-15-1998	
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FOREIGN PATENT DOCUMENTS								
Examiner Initials ¹	Cite No. ¹	Foreign Patent Documents			Name of Patentee or Applicant of Cited Documents	Date of Publication of Cited Document MM-DD-YYYY	Pages, Columns, Lines, Where Relevant Passages or Relevant Figures Appear	T ³
		Office ³	Number ⁴	Kind Code ⁵ (if known)				
			WO/9915626		Greenwald et al.	04-1999		RECEIVED

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JP	1	ANDRADE, et al. "Automatic extraction of keywords from scientific text: Application to the knowledge domain of protein families", <i>Bioinformatics</i> , (1998) Vol. 14(7): 600-60.	
JP		ANDRADE, et al. "Automated extraction of information in molecular biology", <i>FEBS</i> , (2000) Vol. 476: 12-17.	
JP		BECKER, et al. "A graph layout algorithm for drawing metabolic pathways", <i>Bioinformatics</i> , (2001) Vol. 17(5): 461-467.	
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JP		FRIEDMAN, et al. "Genies: A natural-language processing system for the extraction of molecular pathways from journal articles", <i>Bioinformatics</i> , (2001) Vol. 17(Suppl. 1): S74-S82.	

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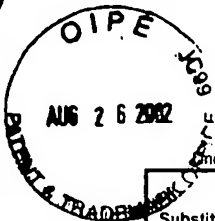
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sp		FUKUDA, et al. "Toward information extraction: Identifying protein names from biological papers", <i>Proc. of the Pacific Symposium on Biocomputing</i> (1998): 707-719.	
sp		FUKUDA, et al. "Knowledge representation of signal transduction", <i>Bioinformatics</i> , (2001) Vol. 17(9): 829-837.	
sp		HUA et al., "Construction of a modular yeast two hybrid cDNA library from human EST clones for the human genome protein linkage map," <i>Gene</i> , 1998, vol. 215, no. 1, pp. 143-152.	
sp		HISHIKI, et al. "Developing NLP tools for genome informatics: An information extraction perspective", <i>Genome Informatics</i> , (1998) Vol. 9: 81-90.	
sp		HUMPHREYS, et al. "Automatically extracting enzyme interaction and protein structure information from Biological Science journal articles", <i>Proc. of the Symposium on Artificial Intelligence in Bioinformatics of the 2000 Convention of the Society for the Study of Artificial Intelligence and the Simulation of Behaviour</i> , (2000) (AISB-00), Birmingham, UK: 17-20.	
sp		INGRAM et al., "Developing mouse models of aging: a consideration of strain differences in age-related behavioral and neural parameters," <i>Neurobiology of Aging</i> , 1999, vol. 20, no. 2, pp. 137-145.	
sp		KRAUTHAMMER, et al. "Using BLAST for identifying gene and protein names in journal articles", <i>Gene</i> , (2000) Vol. 259: 245-252.	
sp		MARCOTTE, et al. "Mining literature for protein-protein interactions", <i>Bioinformatics</i> , (2001) Vol. 17(4): 359-363.	
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sp		NEVILL-MANNING, Craig G., "Highly Specific Protein Sequence Motifs for Genome Analysis", Colloquium Paper, <i>Proc. Natl. Acad. Sci. USA</i> , (1998), Vol. 95, pp. 5865-5871	
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sp		ONO, et al. "Automated extraction of information on protein-protein interactions from the biological literature", <i>Bioinformatics</i> , (2001) Vol. 17(2): 155-161.	

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sp		PROUX, et al. "Detecting gene symbols and names in biological texts: A first step toward pertinent information extraction", <i>Genome Inf.</i> , Vol. 9: 72-80 (1988).	
sp		RAYCHAUDHURI, et al. "Basic microarray analysis: Grouping and feature reduction", <i>Trends in Biotechnology</i> , (2001) Vol. 19(5): 189-193.	
sp		RAYCHAUDHURI, et al. "Associating genes with gene ontology codes using a maximum entropy analysis of biomedical literature", <i>Genome Res.</i> (2002) Vol. 12: 203-214.	
sp		RINDFLESCH, et al. "Mining molecular binding terminology from biomedical text", <i>Proc. AMIA Symposium</i> , (1999): 127-131.	
sp		SALAMONSEN, et al. "BioJAKE: A tool for the creation, visualization, and manipulation of metabolic pathways", <i>Proc. of the Pacific Symposium on Biocomputing 1999</i> , (1999).	
sp		SEKIMIZU, et al. "Identifying the interaction between genes and gene products based on frequently seen verbs in Medline abstracts", <i>Genome Inf.</i> , (1998) Vol. 9: 62-71	
sp		SCHATZ. "Information retrieval in digital libraries: Bringing search to the net", <i>Science</i> , (1997) Vol. 275(5298): 327-334.	
sp		STEPHENS, et al. "Detecting gene relationships from Medline abstracts", <i>Proc. of the Pacific Symposium on Biocomputing</i> , (2001): 483-495.	
sp		TAMAYO, et al. "Interpreting patterns of gene expression with self-organizing maps: Methods and application to hematopoietic differentiation", <i>Proc. Natl. Acad. Sci. USA</i> , (1999) Vol. 96: 2907-2912.	
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